Amendments t the Claims:

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

1. (currently amended) A method for the amplification of a population of nucleic acids comprising a population of poly(A)+ RNA, wherein said method preserves the relative abundance of individual nucleic acid species, said method comprising:

a first step of mixing said population of nucleic acids with a primer comprising oligo-dT in a single reaction vessel under conditions that allow hybridization of said primer with said population of poly(A)+ RNA;

a second step of synthesizing a single-stranded DNA population from said population of poly(A)+ RNA wherein a reverse transcriptase, dNTPs and a first buffer are added to the single reaction vessel to synthesize said single-stranded DNA population;

a third step of synthesizing a population of double-stranded DNA from said single-stranded DNA population wherein a second buffer, different from said first buffer, and a four enzyme-mix comprising a DNA polymerase are added to said single reaction vessel to synthesize said double-stranded cDNA and wherein the reaction is incubated at about 16 °C for at least about 2 hours followed by heating to about 75°C for at least 1 minute; and

a fourth step of synthesizing multiple copies of RNA from said double-stranded DNA population, wherein an RNA polymerase and a third buffer, different from said first

and second buffers, are added to said single reaction vessel to synthesize said multiple copies of RNA.

Claim 2. (canceled)

Claim 3. (original) The method of claim 1, wherein said nucleic acid is selected from the group consisting of genomic DNA, cDNA, total RNA, poly(A)$^+$ RNA, and oligonucleotides.

Claim 4. (original) The method of claim 3, wherein said poly(A)$^+$ RNA is mRNA.

Claim 5. (original) The method of claim 1, further comprising:

contacting said multiple copies of RNA with a solid support comprising nucleic acid probes.

Claim 6. (original) The method of claim 5, further comprising:

detecting the presence or absence of hybridization of said multiple copies of RNA to said nucleic acid probes on said solid support.

Claim 7. (original) The method of claim 5, wherein said solid support comprising nucleic acid probes is selected from the group consisting of a nucleic acid probe array, a membrane blot, a microwell, a bead, and a sample tube.

Claim 8. (original) The method of claim 1, wherein said nucleic acid is isolated from an eukaryotic cell or tissue.

Claim 9. (original) The method of claim 8, wherein said eukaryotic cell or tissue is mammalian.

Claim 10. (original) The method of claim 9, wherein said mammalian cell or tissue is human.

Claim 11. (original) The method of claim 1, wherein said nucleic acid is isolated from a source selected from the group consisting of dissected tissue, microdissected tissue, a tissue subregion, a tissue biopsy sample, a cell sorted population, a cell culture, and a single cell.

Claim 12. (original) The method of claim 1, wherein said nucleic acid is isolated from a cell or tissue source selected from the group consisting of brain, liver, heart, kidney, lung, spleen, retina, bone, lymph node, endocrine gland, reproductive organ, blood, nerve, vascular tissue, and olfactory epithelium.

Claim 13. (original) The method of claim 1, wherein said nucleic acid is isolated from a cell or tissue source selected from the group consisting of embryonic and tumorigenic.

Claims 14-19. (canceled)

Claim 20. (previously presented) The method of claim 1, wherein at least one step of synthesizing comprises the use of an automated machine.

Claim 21. (currently amended) The method of claim 20, wherein said automated machine is selected from the group consisting of a PCR thermocycler, an integrated reaction device, and a robotic delivery system ~~sytem~~.

Claims 22-24. (canceled)

Claim 25. (previously presented) The method of claim 1, wherein said four-enzyme mix further comprises enzymes selected from the group consisting of DNA polymerase, RNA polymerase, reverse transcriptase, terminal transferase, ligase and RNase.

Claim 26. (previously presented) The method of claim 1 wherein the DNA polymerase is thermal-stable.